A)

|  | $a$ | $b$ | $c$ | $d$ | $e$ | $f$ | $g$ | $h$ | $i$ | $j$ | $k$ | $l$ | $m$ | $n$ | $o$ | $p$ |
| :--- | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| PB $N_{\text {eq }}$ | 1.89 | 2.08 | 1.89 | 1.40 | 2.07 | 1.73 | 4.95 | 1.99 | 2.01 | 3.44 | 1.72 | 1.96 | 1.31 | 2.08 | 2.39 | 2.67 |
| av. $N_{\text {eq }}$ | 1.29 | 1.38 | 1.30 | 1.14 | 1.40 | 1.24 | 2.04 | 1.37 | 1.36 | 1.71 | 1.27 | 1.29 | 1.12 | 1.40 | 1.55 | 1.79 |

B)


Sup data 7. Analysis of Protein Blocks' Neq. PB $N_{\text {eq }}$ is the $N_{\text {eq }}$ directly computed from the PB frequencies observed (see Figure 4) while average $N_{\text {eq }}$ is the mean values of observed $N_{\text {eq }}$ at each residue (position) associated to a given PB. The information is so different as the first one is the sum of the behaviours of every PB during dynamics ( 16 values) while the second is the mean values of thousands of different positions observed individually. Are provided A) the values and B) illustrative plot with a zoom on the smallest values. The Pearson coefficient is of 0.94 .

